



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 857 896

Source: OIPE

Date Processed by STIC: 09 24 2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09 857 896

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length. Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused file <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (1) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ☒ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

[illegible]

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,896

DATE: 09/24/2001

TIME: 16:33:18

Input Set : A:\BB1313 PCT Seq List.txt

Output Set : N:\CRF3\09242001\I857896.raw

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60      1          5          10          15
62 Ser Thr Ile Pro Leu Val Val Thr Leu Ala Val Gly Thr Lys Leu Gln
63      20          25          30
65 Ala Ile Ile Ala Met Met Ala Val Glu Ile Lys Glu Arg His Thr Val
66      35          40          45
68 Ile Gln Gly Met Pro Val Val Lys Leu Ser Asp Glu His Phe Trp Phe
69      50          55          60
71 Gly Lys Pro Arg Leu Val Leu His Leu Ile His Phe Ala Ser Phe Gln
72      65          70          75          80
74 Asn Ala Phe Glu Ile Thr Tyr Phe Phe Trp Ile Trp Tyr Glu Phe Gly
75      85          90          95
77 Leu Arg Ser Cys Phe His Asp Asn Phe Glu Leu Ile Ile Ala Arg Val
78      100          105          110
80 Cys Leu Gly Val Val Val Gln Phe Met Cys Ser Tyr Ile Thr Leu Pro
81      115          120          125
83 Leu Tyr Ala Leu Val Ser Gln Met Gly Ser Gln Met Lys Arg Thr Ile
84      130          135          140
86 Phe Asp Glu Gln Thr Ala Lys Ala Leu Lys Lys Trp His Lys Ala Ala
87      145          150          155          160
89 Val Val Lys Lys Lys Gln Gln Lys Gly Ser Ser His Glu Pro Gly Ser
90      165          170          175
92 Glu Thr Pro Gly Thr Glu Thr Thr Thr Thr Thr Ala Thr Ala Thr Glu
93      180          185          190
95 Glu Ser Gln Arg Glu Arg Asp Ala Ala Ala Met Pro Val Arg His Leu
96      195          200          205
98 His Arg Tyr Lys Thr Ile Ala His Val Gly Ala Thr Gly Thr Leu Ser
99      210          215          220
101 Asp Ser Asp Cys Ser Asp Thr Asp Thr Pro Phe Ala Ser Pro Thr Arg
102      225          230          235          240
104 Leu Leu Ile Pro Pro Thr Lys Gln Arg Ser Leu Asp Ala Gly Arg Ala
105      245          250          255
107 Glu Val Arg Val Asp Val Asp Ser Thr Pro Thr Pro Thr Pro Glu
108      260          265          270
110 Arg His Asp Ser Phe Ser Phe Pro Arg Leu Pro Ala His Asn Leu Gln
111      275          280          285
113 Gln Lys
114      290
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 501
118 <212> TYPE: DNA
119 <213> ORGANISM: Oryza sativa
121 <220> FEATURE:
122 <221> NAME/KEY: unsure
123 <222> LOCATION: (335)
125 <220> FEATURE:
126 <221> NAME/KEY: unsure
127 <222> LOCATION: (415)
129 <220> FEATURE:
130 <221> NAME/KEY: unsure

```

FYI: It is mandatory that you list
 which nucleotide bases are possible
 values for your unknowns in field 223
 in the form
 "n is any nucleotide nucleotide"
 or "n is a a c c o r t" or in
 some similar fashion.

RAW SEQUENCE LISTING
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Input Set : A:\BB1313 PCT Seq List.txt
Output Set : N:\CRF3\09242001\I857896.raw

131 <222> LOCATION: (455)
133 <220> FEATURE:
134 <221> NAME/KEY: unsure
135 <222> LOCATION: (479)
137 <220> FEATURE:
138 <221> NAME/KEY: unsure
139 <222> LOCATION: (482)
141 <220> FEATURE:
142 <221> NAME/KEY: unsure
143 <222> LOCATION: (493)
145 <400> SEQUENCE: 3
146 aaaattttctc tcccgcgact ctctacgcgg cggcgtgcac gttctcctcc acctccgtgc 60
147 actattttaact tcccagtttg agtttgacat tctcgcggga agaaggagaa gaagttgggtg 120
148 agcctgtgag aggcgtgattg cgcgcgggcc atggccggag ggggagggaa ggcggcgccg 180
149 ggcgcggcgcg aagcgcgggc gataacgctg gaggcacacac cgacgtggat cgtctccgcc 240
150 gtcctgcttcg tcatcgtcat catctcgtctg ctcttcgagc gctcgtccca ccgctcgccg 300
W--> 151 aagaaggttga agaagacgcg aagaaccgct ctacnaggga ccctcaagtc aaagaagact 360
W--> 152 gatgctgctg gggcatctc gctcgtcgtg aagttccag ggtgcacga gaaghnagctg 420
W--> 153 aagcaacctga tggacactgc agcctcaact cgaacthagg cccaagacgc aagacacgnc 480
W--> 154 anggcgcgcc ggntgagagt c Errorcd 501
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 31
158 <212> TYPE: PRT
159 <213> ORGANISM: Oryza sativa
161 <220> FEATURE:
162 <221> NAME/KEY: UNSURE
163 <222> LOCATION: (62)
165 <400> SEQUENCE: 4
166 Met Ala Gly Gly Gly Lys Ala Ala Ala Gly Gly Gly Glu Ala Pro
167 1 5 10 15
169 Ala Ile Thr Leu Glu His Thr Pro Thr Trp Ile Val Ser Ala Val Cys
170 20 25 30
172 Phe Val Ile Val Ile Ile Ser Leu Leu Phe Glu Arg Leu Leu His Arg
173 35 40 45
W--> 175 Leu Gly Lys Arg Leu Lys Lys Thr Ala Arg Thr Ala Leu Xaa Gly Thr
176 50 55 60
178 Leu Lys Ser Lys Lys Thr Asp Ala Ala Gly Val Ile Ser Leu Leu Leu
179 65 70 75 80
181 Lys
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 513
186 <212> TYPE: DNA
187 <213> ORGANISM: Oryza sativa
189 <220> FEATURE:
190 <221> NAME/KEY: unsure
191 <222> LOCATION: (425)
193 <220> FEATURE:
194 <221> NAME/KEY: unsure
195 <222> LOCATION: (492)

Errored:
Location: 455 is not represented as an
unknown in the actual gene sequence.
E. Location 445 represented as an unknown
in the gene sequence is not described
in field 222.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,896

DATE: 09/24/2001

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Input Set : A:\BB1313 PCT Seq List.txt

Output Set: N:\CRF3\09242001\I857896.raw

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197 <220> FEATURE:
198 <221> NAME/KEY: unsure
199 <222> LOCATION: (507)
201 <400> SEQUENCE: 5
202 acagatggga tcaaacatga agaagaccat ctcgaggag cagacgatga aggcocctgat 60
203 gaactggagg aagacggcga gggagaagaa gaagctccgg gacgccgacg agttcctagc 120
204 acagatgagc ggcgacacga cgccgagccg cggtctgctg ccggtgcacc tgctgcacaa 180
205 gcaaaagggtg aggtcggaag atcccgccag cgcaccggca tcgccggggt tcgccggaga 240
206 ggccagggac atgtaccggg tgcccgtggc gccggtgggt cggccgcatg ggtttaaccg 300
207 gatggaccgg gataagagga gggcgcgctc ctgcctggcc atccaagtgt acatcgccga 360
208 ttctgatttc tccttcagtg tacaacgggt atggccgaaa ggtttctctg tacttaaaat 420
W--> 209 tgtanagcag caaatatagg aagtacaagt tatagttggt acactacata tagaggattt 480
W--> 210 agaaaagttc antcgatttt ttttaagnaac aat 513
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 129
214 <212> TYPE: PRT
215 <213> ORGANISM: Oryza sativa
217 <400> SEQUENCE: 6
218 Gln Met Gly Ser Asn Met Lys Lys Thr Ile Phe Glu Glu Gln Thr Met
219 1 5 10 15
221 Lys Ala Leu Met Asn Trp Arg Lys Thr Ala Arg Glu Lys Lys Lys Leu
222 20 25 30
224 Arg Asp Ala Asp Glu Phe Leu Ala Gln Met Ser Gly Asp Thr Thr Pro
225 35 40 45
227 Ser Arg Gly Ser Ser Pro Val His Leu Leu His Lys Gln Arg Val Arg
228 50 55 60
230 Ser Glu Asp Pro Pro Ser Ala Pro Ala Ser Pro Gly Phe Ala Gly Glu
231 65 70 75 80
233 Ala Arg Asp Met Tyr Pro Val Pro Val Ala Pro Val Val Arg Pro His
234 85 90 95
236 Gly Phe Asn Arg Met Asp Pro Asp Lys Arg Arg Ala Ala Ser Ser Ser
237 100 105 110
239 Ala Ile Gln Val Asp Ile Ala Asp Ser Asp Phe Ser Phe Ser Val Gln
240 115 120 125
242 Arg
245 <210> SEQ ID NO: 7
246 <211> LENGTH: 1745
247 <212> TYPE: DNA
248 <213> ORGANISM: Glycine max
250 <400> SEQUENCE: 7
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252 agttcaactcc gacgtggggt gtggccgcct ttgcacagt catcgctgcc atttccctcg 120
253 ccgctgagcg cctccttcat tatggcggaag agtttctcaa agccaaggac cagaagccgc 180
254 tctacgaagc tctccagaag atcaagaaga agctgatgct ttgggggttc atttccctcg 240
255 ttttgacggt tacacaaaac ggcattacca aaatctcggt tcgacctctc ttgacgctcc 300
256 acatgcctcc gtgtaacttc cagcagcctc cagcaaacca cgaatctcat ttccagacat 360
257 ttttccctgg aacagccagg cgcttctctc ctggggaaca ctccaacccc gactcgccct 420
258 ctaaaattgg ttattgctct cgcaagcaca aggtgccttt attatctgtg gaagcaattc 480
259 accaacttca catcttcaatt ttgtctctcg ctgtcgtaca cgtctccttt tccgtgctca 540

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DATE: 09/24/2001

TIME: 16:33:18

Input Set : A:\BB1313 PCT Seq List.txt

Output Set: N:\CRF3\09242001\I857896.raw

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260 ccggtgtctt  tggaggcgcc  agaatacgtc  agtggaaaca  ctgggaagat  tctattgcaa  600
261 aacagaaacta  cgagactgac  cgagttctca  aaccaagggt  cactcaggtt  caccagcatg  660
262 attttatcag  gggctgcttt  gctggttttg  gcaaaagactc  tgctatagtc  ggttggtgtc  720
263 tctcctttct  aaagcaattt  tatggatctg  tgacaaaaac  agattatgtg  acattgcgac  780
264 atgggtttcat  tatgaccac  tgcaggacaa  atccgaagtt  taattttcac  aagtacatga  840
265 tctgtgccct  cgaagatgat  ttcaagcaag  ttgttggtat  aagttgggat  ctttggtctc  900
266 ttgtggttat  ctctctgtta  cttaatatca  atggttgcca  tacgtatttc  tggattgctt  960
267 ttattcctgt  cattctttta  ctgctgtg  gcaactaagct  ggagcacata  ataaccacaac  1020
268 tagctcatga  agtacctgag  aagcatgctg  coatagaagg  tgatttagtt  gtgcagccat  1080
269 cagatgaaca  tttttggtt  catcgcccc  atgttgctct  ctttttgatt  cactttatcc  1140
270 ttttccaaaa  tgcctttgag  atagcatttt  ttttctggat  atgggtcaca  tatggatttg  1200
271 actcctgtat  aatgggacaa  gtctgataca  ttgttccaag  gcttgttatt  ggggtattta  1260
272 ttcaggtact  atgtagctac  agcaccctgc  cactgtatgc  aattgttacg  cagatgggaa  1320
273 ctcaactata  gcgggcaata  tttaatgatc  atttgcaaca  aaacttggt  ggttggggac  1380
274 agaaggcgaa  gaagaggaaa  ggactaaaag  ctgatggcaa  tcttgcccaa  ggaagtcttc  1440
275 aggagagtc  taatacagga  atccagcttg  ggtcaatttt  caagaaggca  actgctccag  1500
276 gagacagttc  ttctgcccc  aaagctgacg  gaatcagctc  agtgtagcta  tttaagttaa  1560
277 gattttacgt  ctatttttgt  aaagttgctc  acagattgca  gtttctctta  tattattttc  1620
278 ttgtctaaca  taatgtagca  ttgtgggaca  tgtgtttgac  ttggtgtacg  cataaggtcg  1680
279 aagtactata  tgagtagatg  ctagtaatgc  tattgtcatt  tctaaaaaaa  aaaaaaaaaa  1740
280 aaaaaa  1745

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283 <211> LENGTH: 506
284 <212> TYPE: PRT
285 <213> ORGANISM: Glycine max
287 <220> FEATURE:
288 <221> NAME/KEY: UNSURE
289 <222> LOCATION: (78)
291 <220> FEATURE:
292 <221> NAME/KEY: UNSURE
293 <222> LOCATION: (97)
295 <220> FEATURE:
296 <221> NAME/KEY: UNSURE
297 <222> LOCATION: (104)
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303 <220> FEATURE:
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305 <222> LOCATION: (262)
307 <220> FEATURE:
308 <221> NAME/KEY: UNSURE
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313 <222> LOCATION: (300)
315 <220> FEATURE:
316 <221> NAME/KEY: UNSURE
317 <222> LOCATION: (302)

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,896

DATE: 09/24/2001

TIME: 16:33:19

Input Set : A:\BB1313 PCT Seq List.txt

Output Set: N:\CRF3\09242001\I857896.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:151 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:152 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:153 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:154 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:209 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:210 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:465 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:466 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:467 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:518 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:521 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:524 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:559 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:656 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:965 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:967 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:967 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:968 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1041 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:1041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1042 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1141 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1143 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

VERIFICATION SUMMARY

DATE: 09/24/2001

PATENT APPLICATION: US/09/857,896

TIME: 16:33:19

Input Set : A:\BB1313 PCT Seq List.txt

Output Set : N:\CRF3\09242001\I857896.raw

L:1144 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1145 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1146 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1185 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1222 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1231 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1243 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1400 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1401 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1402 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1404 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1428 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30
L:1428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1654 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1655 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1657 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1658 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1659 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1660 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1661 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1696 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34
L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1699 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,896

DATE: 09/24/2001

TIME: 16:33:19

Input Set : A:\BB1313 PCT Seq List.txt

Output Set: N:\CRF3\09242001\I857896.raw

L:1699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1702 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34
L:1702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1734 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35
L:1734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35